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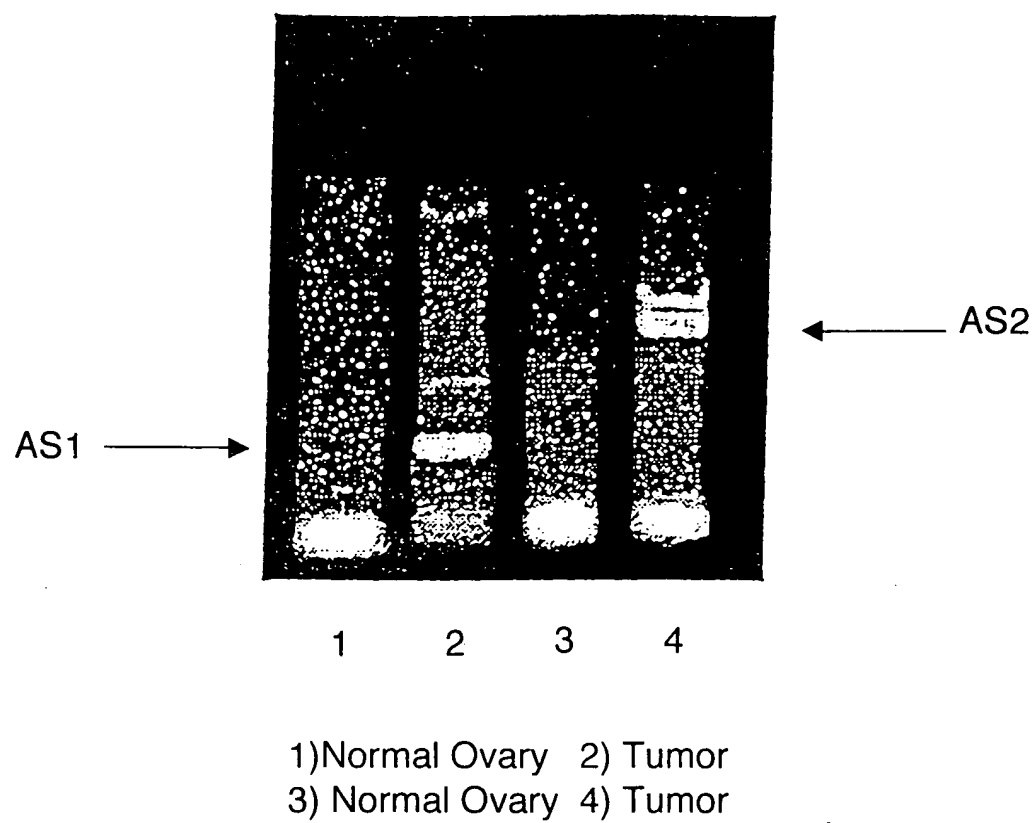


Fig. 1

201	PRIMER				250
Prom	<u>WVLTAAHC</u>	KK	PNLQV...F	LGKHNLRQRE	SSQEQSSVVR
Tadg14	<u>WVVTAAHC</u>	KK	PKYTV...R	LGDHSLQNKD	GPEQEIPVVQ
Try1	<u>WVVSAGHC</u>	YK	SRIQV...R	LGEHNIEVLE	GNEQFINAAK
Scce	<u>WVLTAAHC</u>	KM	NEYTV...H	LGSDTLGDRR	A..QRIKASK
Heps	<u>WVLTAAHC</u>	FP	ERNRVL SRWR	VFAGAVAAQAS	PHGLGLGVQA
					VVYHGGYLF
					300
Prom	...DAASHDQ		<u>DIMLL</u> RLARP	AKLSELIQPL	PLERDCSA..
Tadg14	NSSDVEDHNH		<u>DLMLL</u> QLRDQ	ASLGSKVKPI	SLADHCTQ..
Try1	...DRKTLNN		<u>DIMLI</u> KLSSR	AVINARVSTI	SLPTAPPA..
Scce	ST...QTHVN		<u>DLMLV</u> KLNSQ	ARLSSMVKKV	RLPSRCEP..
Heps	RDPNSEENSN		<u>DIALV</u> HLSSP	LPLTEYIQPV	CLPAAGQALV
					DGKICTVTGM
					350
Prom	GKTAD..GDF		PDTIQCAYIH	LVSREECEHA	..TPGQITQN
Tadg14	GTVTSPRENF		PDTLNCAEVK	IFPQKKCEDA	..YPGQITDG
Try1	GNTASSGADY		PDELQCLDAP	VLSQAKCEAS	..YPGKITSN
Scce	GTTTSPDVTF		PSDLMCVDVK	LISPQDCTKV	..YKDLLENS
Heps	GNTQYYGQQ.		AGVLQEARVP	IIISNDVCNGA	DFYGNQIKPK
					MFCAYPEGG
					351
Prom	<u>KDSCQ</u> GDSGG		SEQ ID No. 1		
Tadg14	ADTCQ GDSGG		SEQ ID No. 2		
Try1	KDSCQ GDSGG		SEQ ID No. 3		
Scce	KNACN GDSGG		SEQ ID No. 4		
Heps	IDACQ GDSGG		SEQ ID No. 5		
					PRIMER

**Fig. 2**

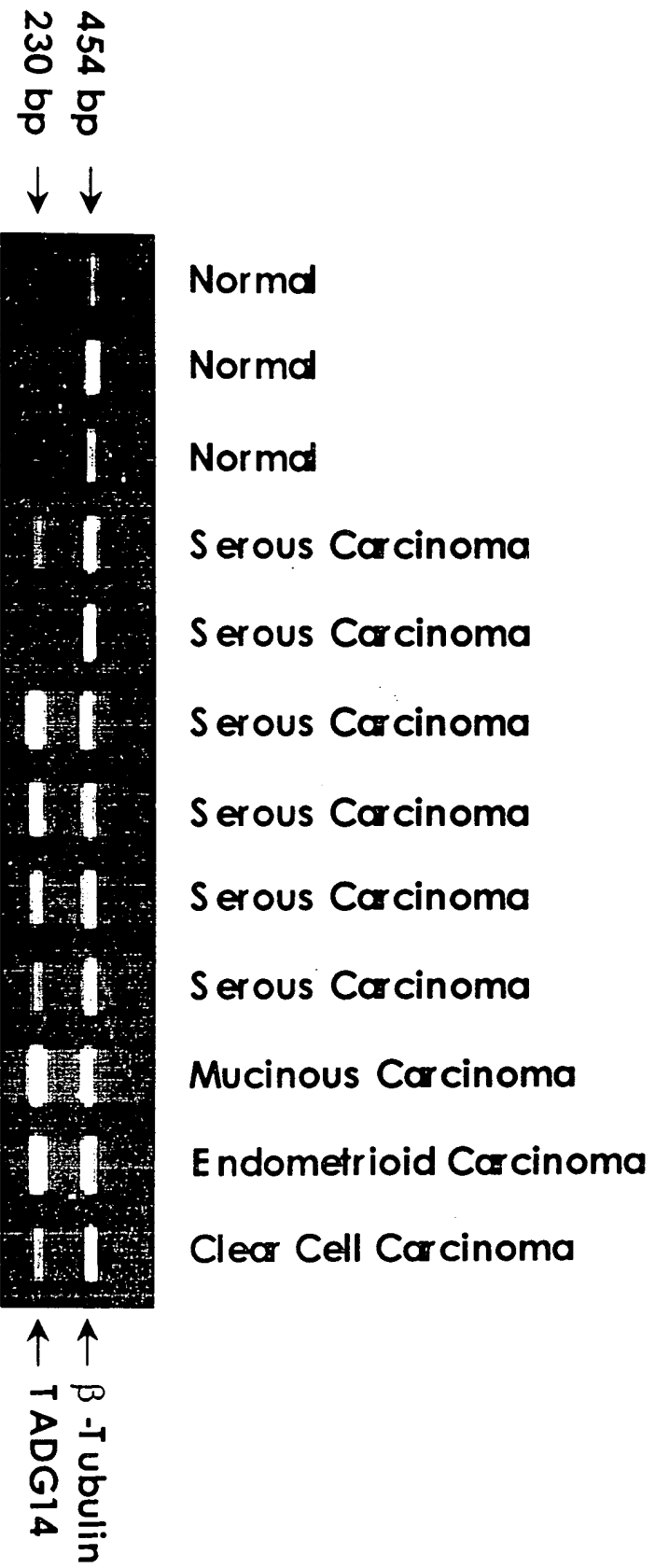


Fig. 3

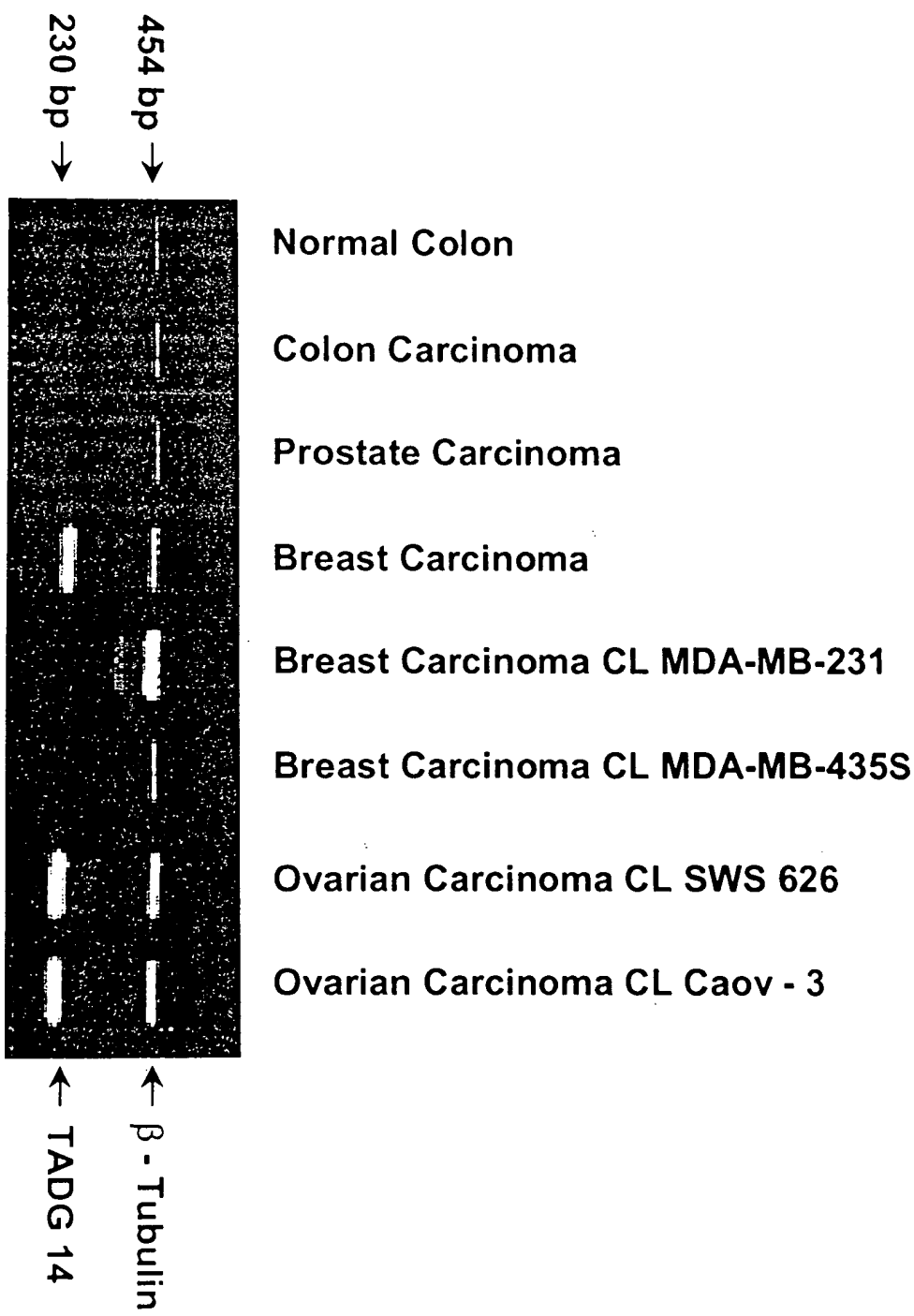


Fig. 4

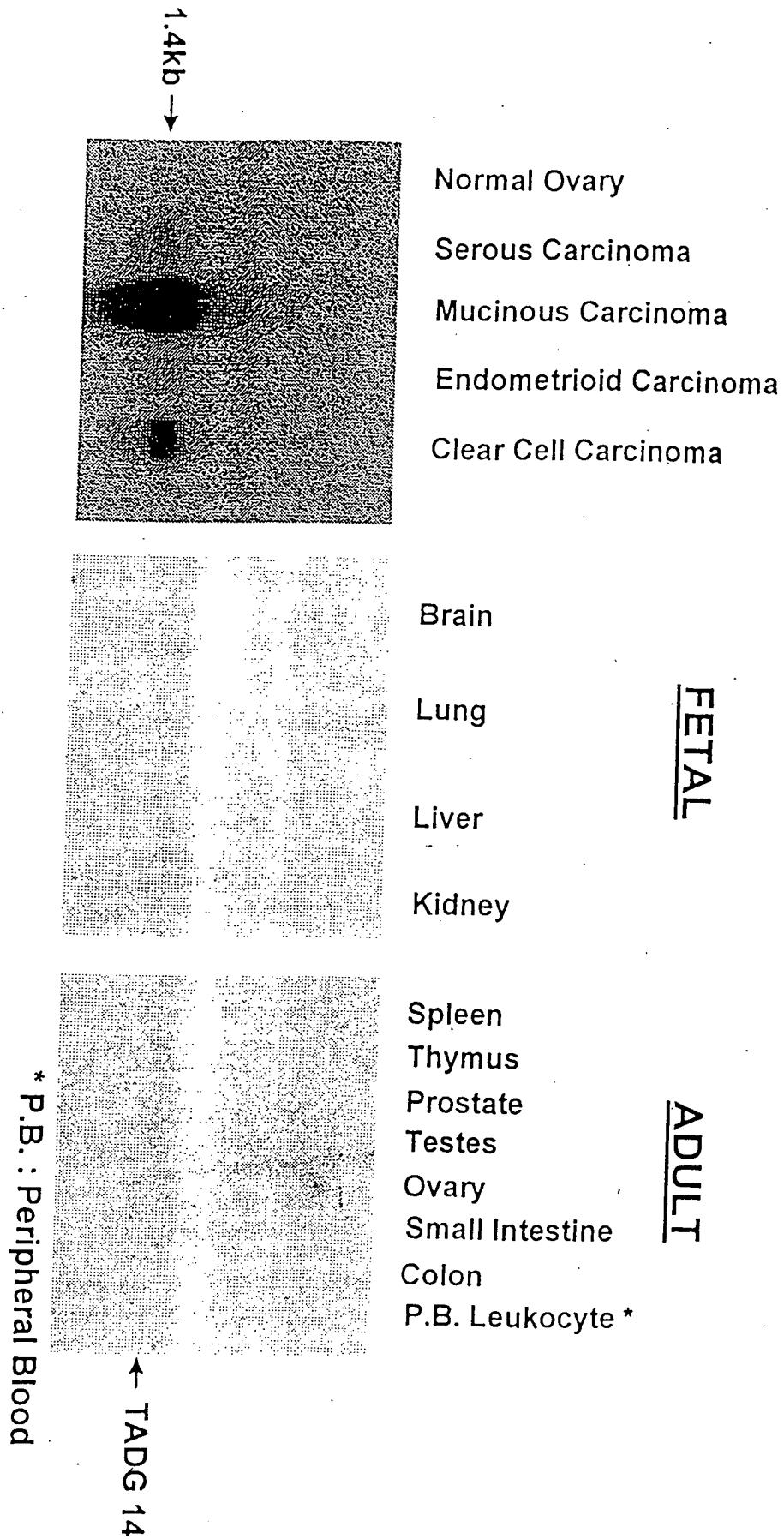


Fig. 5

# Replacement Sheet

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1  CTGTAGCAGGCAGAGCTTACCAAGTCTCTCCGAAC TCAAATGGAAGAAATACCTTATGAA 60
61  TGTAAGAATGTAGGGGGTCATGGCTTGTAATTTACACAGTGTAATGAAACCATCCTAGA 120
121 GGATTATGAGGAATCCTTTCTATGTGATTTTCAATCATAGCAAGCAAGAAAGGCTCCAGT 180
181 GTCAAGGTAGTTCAGCTCTTACAGGATATAAAACAGTCCATACTTGAGAGAAAAAACTTA 240
241 GATCTGAGTGATGGAATGTGAAGCAAATCTTTCAAATCAGTAGACATTTCTTGACATA 300
301 AAACACAGATGAGGAAAGGGCTTCAAATTAGAAGTTACGTAATCACCATCAGAAAGTTCA 360
361 TGTTTGGTAAATTCTGTTACTAGAAATGTAGGAAATTCAGGTATAGCTTTGAATCCCAAT 420
421 TACACATTGGTCAGTGGGAAAATAAGGGCCTCCAACAGGCAAATTCAGGGAGGATAGGT 480
481 TTCAGGGAATGCCCTGGATTCTGGAAGACCTCACCATGGGACGCCCCCGACCTCGTGCGG 540
                                     M G R P R P R A A -
541 CCAAGACGTGGATGTTCTCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCAC 600
      K T W M F L L L L G G A W A G H S R A Q -
601 AGGAGGACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCAGGCGG 660
      E D K V L G G H E C Q P H S Q P W Q A A -
661 CCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAGGTGGCAACTGGGTCC 720
      L F Q G Q Q L L C G G V L V G G N W V L -
721 TTACAGCTGCCCACTGTAAAAAACCGAAATACACAGTACGCCTGGGAGACCACAGCCTAC 780
      T A A H+C K K P K Y T V R L G D H S L Q -
781 AGAATAAAGATGGCCCAGAGCAAGAAATACCTGTGGTTCAGTCCATCCCACACCCCTGCT 840
      N K D G P E Q E I P V V Q S I P H P C Y -
841 ACAACAGCAGCGATGTGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACC 900
      N S S D V E D H N H D+L M L L Q L R D Q -
901 AGGCATCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCAGCCTG 960
      A S L G S K V K P I S L A D H C T Q P G -
961 GCCAGAAGTGCACCGTCTCAGGCTGGGGCACTGTCAACAGTCCCCGAGAGAATTTCTCTG 1020
      Q K C T V S G W G T V T S P R E N F P D -
1021 ACACTCTCAACTGTGCAGAAGTAAAAATCTTTCCCCAGAAGAAGTGTGAGGATGCTTACC 1080
      T L N C A E V K I F P Q K K C E D A Y P -
1081 CGGGGCAGATCACAGATGGCATGGTCTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCC 1140
      G Q I T D G M V C A G S S K G A D T C Q -
1141 AGGGCGATTCTGGAGGCCCTTGGTGTGTGATGGTGCCTCCAGGGCATCACATCCTGGG 1200
      G D S+ G G P L V C D G A L Q G I T S W G -
1201 GCTCAGACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCGCTACC 1260
      S D P C G R S D K P G V Y T N I C R Y L -
1261 TGGACTGGATCAAGAAGATCATAGGCAGCAAGGGCTGATTCTAGGATAAGCACTAGATCT 1320
      D W I K K I I G S K G * SEQ ID No. 6
1321 CCCTTAATAAACTCACGGAATTC SEQ ID No. 7

```

       = Kozak's Consensus sequence

+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

— = Poly - adenylation signal

       = Conserved nt of catalytic triad

○ = aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

Fig. 6

**Fig. 7A**

T14                      SEQ    ID No. 9

**Fig. 7B**



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Tadg14 1 MGRPRPRAAKTWMFLLLLGGAWAGHSRAQEDKVLGGHECQPHSQPWQAAL 50
      |||| | | . |. ||| ||||| .||| |:| || ||||| |||||
Neurop 1 MGRPPPCAIQPWILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAAL 50

      51 FQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPV 100
      |||:|:||||| ||||| ||||| |||.||||| |||.||| |||||
      51 FQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQV 100

      101 VQSIPHPCYNSSDVEDHNNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQ 150
      ||| |||||.|. |||.||:|:|.|. |.|| ||||: |||. |. ||
      101 AQSIQHPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQ 150

      151 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
      || :|||||||.||||-|||||||: | ||| |||||.||:|||||
      151 KCIISGWGTVTSPQENFPNTLNCAEVKIYSQNK CERAYPGKITEGMVCAG 200

      201 SSKGADTCQGDSGGPLVCDGALQGITSWGS DPCGRSDKPGVYTNICRYLD 250
      || ||||| ||||| ||||| ||||| ||||| |||||: : ||||| |||||
      201 SSGADTCQGDSGGPLVCDGMLQGITSWGS DPCGKPEKPGVYTKICRYTT 250

      251 WIKKIIGSKG 260 SEQ ID No. 7
      |||| . .:
      251 WIKKTM DNRD 260 SEQ ID No. 10

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Fig. 8

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